RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10537102_
Source: _PCT_
Date Processed by STIC: _5-1-06_

ENTERED

PCT

Input Set : A:\2006-01-26 0933-0246PUS1.ST25.txt
Output Set: N:\CRF4\05012006\J537102.raw

(pg.6)

```
 3 <110> APPLICANT: Kuja-Panula, Juha
 4        Kiiltomaki, Marjaana
 5        Rauvala, Heikki
 7 <120> TITLE OF INVENTION: NOVEL PROTEIN AND USES THEREOF
 9 <130> FILE REFERENCE: 0933-0246PUS1
11 <140> CURRENT APPLICATION NUMBER: US 10/537,102
12 <141> CURRENT FILING DATE: 2005-06-02
14 <150> PRIOR APPLICATION NUMBER: US 60/433,011
15 <151> PRIOR FILING DATE: 2002-12-13
17 <160> NUMBER OF SEQ ID NOS: 79
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1479
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1479)
30 <400> SEQUENCE: 1
31 atg cac ccc cac cgt gac ccg aga ggc ctc tgg ctc ctg ctg ccg tcc    48
32 Met His Pro His Arg Asp Pro Arg Gly Leu Trp Leu Leu Leu Pro Ser
33  1               5                  10                  15
35 ttg tcc ctg ctg ctt ttt gag gtg gcc aga gct ggc cga gcc gtg gtt    96
36 Leu Ser Leu Leu Leu Phe Glu Val Ala Arg Ala Gly Arg Ala Val Val
37             20                  25                  30
39 agc tgt cct gcc gcc tgc ttg tgc gcc agc aac atc ctc agc tgc tcc   144
40 Ser Cys Pro Ala Ala Cys Leu Cys Ala Ser Asn Ile Leu Ser Cys Ser
41         35                  40                  45
43 aag cag cag ctg ccc aat gtg ccc cat tcc ttg ccc agt tac aca gca   192
44 Lys Gln Gln Leu Pro Asn Val Pro His Ser Leu Pro Ser Tyr Thr Ala
45     50                  55                  60
47 cta ctg gac ctc agt cac aac aac ctg agc cgc ctg cgg gcc gag tgg   240
48 Leu Leu Asp Leu Ser His Asn Asn Leu Ser Arg Leu Arg Ala Glu Trp
49 65                  70                  75                  80
51 acc ccc acg cgc ctg acc caa ctg cac tcc ctg ctg ctg agc cac aac   288
52 Thr Pro Thr Arg Leu Thr Gln Leu His Ser Leu Leu Leu Ser His Asn
53                 85                  90                  95
55 cac ctg aac ttc atc tcc tct gag gcc ttt tcc ccg gta ccc aac ctg   336
56 His Leu Asn Phe Ile Ser Ser Glu Ala Phe Ser Pro Val Pro Asn Leu
57             100                 105                 110
59 cgc tac ctg gac ctc tcc tcc aac cag ctg cgt aca ctg gat gag ttc   384
60 Arg Tyr Leu Asp Leu Ser Ser Asn Gln Leu Arg Thr Leu Asp Glu Phe
61             115                 120                 125
```

```
 63 ctg ttc agt gac ctg caa gta ctg gag gtg ctg ctg ctc tac aat aac    432
 64 Leu Phe Ser Asp Leu Gln Val Leu Glu Val Leu Leu Leu Tyr Asn Asn
 65     130                 135                 140
 67 cac atc atg gcg gtg gac cgg tgc gcc ttc gat gac atg gcc cag ctg    480
 68 His Ile Met Ala Val Asp Arg Cys Ala Phe Asp Asp Met Ala Gln Leu
 69 145                 150                 155                 160
 71 cag aaa ctc tac ttg agc cag aac cag atc tct cgc ttc cct ctg gaa    528
 72 Gln Lys Leu Tyr Leu Ser Gln Asn Gln Ile Ser Arg Phe Pro Leu Glu
 73                 165                 170                 175
 75 ctg gtc aag gaa gga gcc aag cta ccc aaa cta acg ctc ctg gat ctc    576
 76 Leu Val Lys Glu Gly Ala Lys Leu Pro Lys Leu Thr Leu Leu Asp Leu
 77                 180                 185                 190
 79 tct tct aac aag ctg aag aac ttg cca ttg cct gac ctg cag aag ctg    624
 80 Ser Ser Asn Lys Leu Lys Asn Leu Pro Leu Pro Asp Leu Gln Lys Leu
 81             195                 200                 205
 83 ccg gcc tgg atc aag aat ggg ctg tac cta cat aac aac ccc ctg aac    672
 84 Pro Ala Trp Ile Lys Asn Gly Leu Tyr Leu His Asn Asn Pro Leu Asn
 85     210                 215                 220
 87 tgc gac tgt gag ctc tac cag ctg ttt tca cac tgg cag tat cgg cag    720
 88 Cys Asp Cys Glu Leu Tyr Gln Leu Phe Ser His Trp Gln Tyr Arg Gln
 89 225                 230                 235                 240
 91 ctg agc tcc gtg atg gac ttt caa gag gat ctg tac tgc atg aac tcc    768
 92 Leu Ser Ser Val Met Asp Phe Gln Glu Asp Leu Tyr Cys Met Asn Ser
 93                 245                 250                 255
 95 aag aag ctg cac aat gtc ttc aac ctg agt ttc ctc aac tgt ggc gag    816
 96 Lys Lys Leu His Asn Val Phe Asn Leu Ser Phe Leu Asn Cys Gly Glu
 97             260                 265                 270
 99 tac aag gag cgt gcc tgg gag gcc cac ctg ggt gac acc ttg atc atc    864
100 Tyr Lys Glu Arg Ala Trp Glu Ala His Leu Gly Asp Thr Leu Ile Ile
101             275                 280                 285
103 aag tgt gac acc aag cag caa ggg atg acc aag gtg tgg gtg aca cca    912
104 Lys Cys Asp Thr Lys Gln Gln Gly Met Thr Lys Val Trp Val Thr Pro
105     290                 295                 300
107 agt aat gaa cgg gtg cta gat gag gtg acc aat ggc aca gtg agt gtg    960
108 Ser Asn Glu Arg Val Leu Asp Glu Val Thr Asn Gly Thr Val Ser Val
109 305                 310                 315                 320
111 tct aag gat ggc agt ctt ctt ttc cag cag gtg cag gtc gag gac ggt    1008
112 Ser Lys Asp Gly Ser Leu Leu Phe Gln Gln Val Gln Val Glu Asp Gly
113             325                 330                 335
115 ggt gtg tat acc tgc tat gcc atg gga gag act ttc aat gag aca ctg    1056
116 Gly Val Tyr Thr Cys Tyr Ala Met Gly Glu Thr Phe Asn Glu Thr Leu
117             340                 345                 350
119 tct gtg gaa ttg aaa gtg cac aat ttc acc ttg cac gga cac cat gac    1104
120 Ser Val Glu Leu Lys Val His Asn Phe Thr Leu His Gly His His Asp
121             355                 360                 365
123 acc ctc aac aca gcc tat acc acc cta gtg ggc tgt atc ctt agt gtg    1152
124 Thr Leu Asn Thr Ala Tyr Thr Thr Leu Val Gly Cys Ile Leu Ser Val
125     370                 375                 380
127 gtc ctg gtc ctc ata tac cta tac ctc acc cct tgc cgc tgc tgg tgc    1200
```

RAW SEQUENCE LISTING   DATE: 05/01/2006
PATENT APPLICATION: US/10/537,102   TIME: 11:01:26

Input Set : A:\2006-01-26 0933-0246PUS1.ST25.txt
Output Set: N:\CRF4\05012006\J537102.raw

```
128 Val Leu Val Leu Ile Tyr Leu Tyr Leu Thr Pro Cys Arg Cys Trp Cys
129 385                 390                 395                 400
131 cgg ggt gta gag aag cct tcc agc cat caa gga gac agc ctc agc tct     1248
132 Arg Gly Val Glu Lys Pro Ser Ser His Gln Gly Asp Ser Leu Ser Ser
133             405             410             415
135 tcc atg ctt agt acc aca ccc aac cat gat cct atg gct ggt ggg gac     1296
136 Ser Met Leu Ser Thr Thr Pro Asn His Asp Pro Met Ala Gly Gly Asp
137             420             425             430
139 aaa gat gat ggt ttt gac cgg cgg gtg gct ttc ctg gaa cct gct gga     1344
140 Lys Asp Asp Gly Phe Asp Arg Arg Val Ala Phe Leu Glu Pro Ala Gly
141             435             440             445
143 cct ggg cag ggt caa aac ggc aag ctc aag cca ggc aac acc ctg cca     1392
144 Pro Gly Gln Gly Gln Asn Gly Lys Leu Lys Pro Gly Asn Thr Leu Pro
145         450             455             460
147 gtg cct gag gcc aca ggc aag ggc caa cgg agg atg tcg gat cca gaa     1440
148 Val Pro Glu Ala Thr Gly Lys Gly Gln Arg Arg Met Ser Asp Pro Glu
149 465             470             475             480
151 tca gtc agc tcg gtc ttc tct gat acg ccc att gtg gtg               1479
152 Ser Val Ser Ser Val Phe Ser Asp Thr Pro Ile Val Val
153             485             490
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 493
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
161 <400> SEQUENCE: 2
162 Met His Pro His Arg Asp Pro Arg Gly Leu Trp Leu Leu Leu Pro Ser
163   1               5                 10                  15
165 Leu Ser Leu Leu Leu Phe Glu Val Ala Arg Ala Gly Arg Ala Val Val
166             20                  25                  30
168 Ser Cys Pro Ala Ala Cys Leu Cys Ala Ser Asn Ile Leu Ser Cys Ser
169         35                  40                  45
171 Lys Gln Gln Leu Pro Asn Val Pro His Ser Leu Pro Ser Tyr Thr Ala
172     50                  55                  60
174 Leu Leu Asp Leu Ser His Asn Asn Leu Ser Arg Leu Arg Ala Glu Trp
175 65                  70                  75                  80
177 Thr Pro Thr Arg Leu Thr Gln Leu His Ser Leu Leu Leu Ser His Asn
178             85                  90                  95
180 His Leu Asn Phe Ile Ser Ser Glu Ala Phe Ser Pro Val Pro Asn Leu
181             100                 105                 110
183 Arg Tyr Leu Asp Leu Ser Ser Asn Gln Leu Arg Thr Leu Asp Glu Phe
184         115                 120                 125
186 Leu Phe Ser Asp Leu Gln Val Leu Glu Val Leu Leu Leu Tyr Asn Asn
187     130                 135                 140
189 His Ile Met Ala Val Asp Arg Cys Ala Phe Asp Asp Met Ala Gln Leu
190 145                 150                 155                 160
192 Gln Lys Leu Tyr Leu Ser Gln Asn Gln Ile Ser Arg Phe Pro Leu Glu
193             165                 170                 175
195 Leu Val Lys Glu Gly Ala Lys Leu Pro Lys Leu Thr Leu Leu Asp Leu
196             180                 185                 190
```

```
198 Ser Ser Asn Lys Leu Lys Asn Leu Pro Leu Pro Asp Leu Gln Lys Leu
199         195                 200                 205
201 Pro Ala Trp Ile Lys Asn Gly Leu Tyr Leu His Asn Asn Pro Leu Asn
202     210                 215                 220
204 Cys Asp Cys Glu Leu Tyr Gln Leu Phe Ser His Trp Gln Tyr Arg Gln
205 225                 230                 235                 240
207 Leu Ser Ser Val Met Asp Phe Gln Glu Asp Leu Tyr Cys Met Asn Ser
208                 245                 250                 255
210 Lys Lys Leu His Asn Val Phe Asn Leu Ser Phe Leu Asn Cys Gly Glu
211             260                 265                 270
213 Tyr Lys Glu Arg Ala Trp Glu Ala His Leu Gly Asp Thr Leu Ile Ile
214         275                 280                 285
216 Lys Cys Asp Thr Lys Gln Gln Gly Met Thr Lys Val Trp Val Thr Pro
217     290                 295                 300
219 Ser Asn Glu Arg Val Leu Asp Glu Val Thr Asn Gly Thr Val Ser Val
220 305                 310                 315                 320
222 Ser Lys Asp Gly Ser Leu Leu Phe Gln Gln Val Gln Val Glu Asp Gly
223             325                 330                 335
225 Gly Val Tyr Thr Cys Tyr Ala Met Gly Glu Thr Phe Asn Glu Thr Leu
226             340                 345                 350
228 Ser Val Glu Leu Lys Val His Asn Phe Thr Leu His Gly His His Asp
229         355                 360                 365
231 Thr Leu Asn Thr Ala Tyr Thr Thr Leu Val Gly Cys Ile Leu Ser Val
232     370                 375                 380
234 Val Leu Val Leu Ile Tyr Leu Tyr Leu Thr Pro Cys Arg Cys Trp Cys
235 385                 390                 395                 400
237 Arg Gly Val Glu Lys Pro Ser Ser His Gln Gly Asp Ser Leu Ser Ser
238             405                 410                 415
240 Ser Met Leu Ser Thr Thr Pro Asn His Asp Pro Met Ala Gly Gly Asp
241             420                 425                 430
243 Lys Asp Asp Gly Phe Asp Arg Arg Val Ala Phe Leu Glu Pro Ala Gly
244         435                 440                 445
246 Pro Gly Gln Gly Gln Asn Gly Lys Leu Lys Pro Gly Asn Thr Leu Pro
247     450                 455                 460
249 Val Pro Glu Ala Thr Gly Lys Gly Gln Arg Arg Met Ser Asp Pro Glu
250 465                 470                 475                 480
252 Ser Val Ser Ser Val Phe Ser Asp Thr Pro Ile Val Val
253             485                 490
257 <210> SEQ ID NO: 3
258 <211> LENGTH: 1566
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <220> FEATURE:
263 <221> NAME/KEY: CDS
264 <222> LOCATION: (1)..(1566)
266 <400> SEQUENCE: 3
267 atg tcg tta cgt gta cac act ctg ccc acc ctg ctt gga gcc gtc gtc    48
268 Met Ser Leu Arg Val His Thr Leu Pro Thr Leu Leu Gly Ala Val Val
269  1               5                  10                  15
```

```
271 aga ccg ggc tgc agg gag ctg ctg tgt ttg ctg atg atc aca gtg act   96
272 Arg Pro Gly Cys Arg Glu Leu Leu Cys Leu Leu Met Ile Thr Val Thr
273          20              25                  30
275 gtg ggc cct ggt gcc tct ggg gtg tgc ccc acc gct tgc atc tgt gcc   144
276 Val Gly Pro Gly Ala Ser Gly Val Cys Pro Thr Ala Cys Ile Cys Ala
277          35              40                  45
279 act gac atc gtc agc tgc acc aac aaa aac ctg tcc aag gtg cct ggg   192
280 Thr Asp Ile Val Ser Cys Thr Asn Lys Asn Leu Ser Lys Val Pro Gly
281       50                 55                  60
283 aac ctt ttc aga ctg att aag aga ctg gac ctg agt tat aac aga att   240
284 Asn Leu Phe Arg Leu Ile Lys Arg Leu Asp Leu Ser Tyr Asn Arg Ile
285  65                 70                  75                  80
287 ggg ctt ctg gat tct gag tgg att cca gta tcg ttt gca aag ctg aac   288
288 Gly Leu Leu Asp Ser Glu Trp Ile Pro Val Ser Phe Ala Lys Leu Asn
289             85                  90                  95
291 acc cta att ctt cgt cat aac aac atc acc agc att tcc acg ggc agt   336
292 Thr Leu Ile Leu Arg His Asn Asn Ile Thr Ser Ile Ser Thr Gly Ser
293             100                 105                 110
295 ttt tcc aca act cca aat ttg aag tgt ctt gac tta tcg tcc aat aag   384
296 Phe Ser Thr Thr Pro Asn Leu Lys Cys Leu Asp Leu Ser Ser Asn Lys
297          115                 120                 125
299 ctg aag acg gtg aaa aat gct gta ttc caa gag ttg aag gtt ctg gaa   432
300 Leu Lys Thr Val Lys Asn Ala Val Phe Gln Glu Leu Lys Val Leu Glu
301       130                 135                 140
303 gtg ctt ctg ctt tac aac aat cac ata tcc tat ctc gat cct tca gcg   480
304 Val Leu Leu Leu Tyr Asn Asn His Ile Ser Tyr Leu Asp Pro Ser Ala
305 145                 150                 155                 160
307 ttt gga ggg ctc tcc cag ttg cag aaa ctc tac tta agt gga aat ttt   528
308 Phe Gly Gly Leu Ser Gln Leu Gln Lys Leu Tyr Leu Ser Gly Asn Phe
309             165                 170                 175
311 ctc aca cag ttt ccg atg gat ttg tat gtt gga agg ttc aag ctg gca   576
312 Leu Thr Gln Phe Pro Met Asp Leu Tyr Val Gly Arg Phe Lys Leu Ala
313          180                 185                 190
315 gaa ctg atg ttt tta gat gtt tct tat aac cga att cct tcc atg cca   624
316 Glu Leu Met Phe Leu Asp Val Ser Tyr Asn Arg Ile Pro Ser Met Pro
317          195                 200                 205
319 atg cac cac ata aat tta gtg cca gga aaa cag ctg aga ggc atc tac   672
320 Met His His Ile Asn Leu Val Pro Gly Lys Gln Leu Arg Gly Ile Tyr
321       210                 215                 220
323 ctt cat gga aac cca ttt gtc tgt gac tgt tcc ctg tac tcc ttg ctg   720
324 Leu His Gly Asn Pro Phe Val Cys Asp Cys Ser Leu Tyr Ser Leu Leu
325 225                 230                 235                 240
327 gtc ttt tgg tat cgt agg cac ttt agc tca gtg atg gat ttt aag aac   768
328 Val Phe Trp Tyr Arg Arg His Phe Ser Ser Val Met Asp Phe Lys Asn
329             245                 250                 255
331 gat tac acc tgt cgc ctg tgg tct gac tcc agg cac tcg cgt cag gta   816
332 Asp Tyr Thr Cys Arg Leu Trp Ser Asp Ser Arg His Ser Arg Gln Val
333          260                 265                 270
335 ctt ctg ctc cag gat agc ttt atg aat tgc tct gac agc atc atc aat   864
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/01/2006
PATENT APPLICATION: **US/10/537,102**   TIME: 11:01:27

Input Set : **A:\2006-01-26 0933-0246PUS1.ST25.txt**
Output Set: **N:\CRF4\05012006\J537102.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:39; Xaa Pos. 1,3,4,6,8,9,11,13,14,15,16,17,18,19,21,22,24,25,27,28,30
Seq#:39; Xaa Pos. 32,33,35,37,38,39,40,41,42,43,45,46,48,49,51,52,54,56,57
Seq#:39; Xaa Pos. 59,61,62,63,... ,68,63,71,72,74,75,77,79,80,82,84,85
Seq#:39; Xaa Pos. 86,87,88,89,90,91,93,94,96,97,98,100,102,104,105,107,109
Seq#:39; Xaa Pos. 110,111,112,113,114,115,117,118,120,121,123,124,126,128
Seq#:39; Xaa Pos. 129,131,133,134,135,136,137,138,139,141,142,144
Seq#:40; Xaa Pos. 1,4,6,8,9,11,14,15,16,18,19,21,22,23,25,26,27,28
Seq#:41; Xaa Pos. 1,3,6,8,9,11,15,17,18,19,20,21,22,23,25,26,28,29
Seq#:79; Xaa Pos. 2,3,5,7,8,10,11,12,13,14,15,16,17,18,19

```
L:6144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:6148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:16
L:6152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:32
L:6156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:48
L:6160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:64
L:6164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:80
L:6168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:96
L:6172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:112
L:6176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:128
L:6242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:6246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:16
L:6311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:6315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:16
L:6820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
L:6824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:16
```